



Annotated Sheet Showing Changes  
U.S. Application No.: 10/060,990  
Filing Date: January 30, 2002  
Y. Gu, et al. / PB0176  
Human RALGDS-Like Protein 3  
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# Structure of RGL3 and alignment of RasGEFN, RasGEF and RA motifs.

**FIG. 1A**  
RGL3 (710 a.a.)



**FIG. 1**



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**FIG. 1B**  
**RasGEFN motif**

	10	20	30	40	50	60
consensus	..... .....* .....* .....* .....* .....* .....*					
RGL3	1 CKGGLIKGGTLEKLIIEHLTEARDK-VDPTFVETFLITYRSFITTQELLQKLLRYNAIPP	59				
gi 1354501	64 SKVRVLRAARLERLVGELVFGDRE-QDPSFMPAFATYRTFVPTACLLGFLLP--PMPPP	120				
gi 158471	87 RSSRRLRAGTLEALVRHLLDARTAGADMFTPALLATHRAFTSTPALFGLVADRLEALES	146				
gi 544403	636 AGVPMIKGATLCKLIERLTYHIY--ADPTFVRTFLTYYFCSPQQLQLLVERFNIPDP	693				
	111 CKVRTVKAGTLEKLVEHLVPAFQg-SDLSYVTVFLCTYRAFTTTTQQQVLDLLFKRYGCILP	169				
	70	80	90	100	110	120
consensus	.....* .....* .....* .....* .....* .....* .....*					
RGL3	60 EGVE-----D-----IWVKEKVNPRRIQ---NRVLNILRLWV	88				
gi 1354501	121 PPG-----V-----EIKKTAQDLSFNknIRAVVSVLGSWL	152				
gi 158471	147 Y-----PPGELERTT---GVAISVLSTWL	167				
gi 544403	694 SLVygdtgtagaggmgvggDkehknshredwkyRKEYVQp--VQ---FRVLNVLRHWV	748				
	170 Yss-----eDg-----GPQDQLK---NAISSILGTWL	193				
	130	140	150	160		
consensus	.....* .....* .....* .....* .....* .....*					
RGL3	89 ENYWQDFEEDPKLNLFLFEE-FLELVDDK-KYPGLETSIQNILRRLS	132				
gi 1354501	153 QDHPQDFRDHPahsdlgsvrtflgwaapgsaeaqaekllfedflee	198				
gi 158471	168 ASHPEDFGSEVKGQLDRLE-SFLLRTGYaAREGVVGGsADLIRNLR	212				
gi 544403	749 DHHFYDFEKDPMLEKLLN-FLEHVNGK-SMRKWVDSVLKIVQRKN	792				
	194 DQYSEDFCQP-PDFPCLKQlVAYVQLNM-PGSDLERRAHLLLAQLE	237				

**FIG. 1**



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# FIG. 1C

## RasGEF motif

```
consensus 1 LLLLDPKELAEQLTLLDFELFRKIDPSELLGSGVWGRSKKS--PSPL--NLERFIERFNE 56
RGL3      243 LLDfSVDEVAEQTLIDLELFskVRLYECLGSVWSQRDRPGaaGASP--TVRATVAQFNT 300
1BKD_S    171 LLTLHPiEiARQLTLLESDLYRAVQPSelVGSVWTKEDKEI--NSP---NLLKMIRHTTN 225
gi 544403 363 LLLFPpDLVAEQFTLMDAELFKKVVPPYHCLGSIWSQRAKKG--KEHlaptIRATVAQFNN 420
gi 6919956 239 VLvFLADHLAEQLTLLDAELFLNLIPsQCLGGLGHDRDPG--HSHlcpSVRATVTQFNK 296

consensus 70 80 90 100 110 120
.....*.....|.....*.....|.....*.....|.....*.....|.....*.....|
57 VSNWVATEILKQTT-----P--KDAELLskFIQVAKHCRELNNFNLSLMAI 100
RGL3      301 VTGCVLGsvLGAPG-----LaaPQaQRLEKWIRIAQRCRELRNFFSSLRAI 346
1BKD_S    226 LTLWFEKCIvETEN-----L--EERVAVVSRIIEILQVfQELNfNfNGVLEV 269
gi 544403 421 VANCvITTCLGDQSm-----ka--SDRArvVEHWIEVARECRVLKNfSSLYAI 466
gi 6919956 297 VAGAVVSSVLGATStgepggevtirPlP--PQrARLLEKWIRVAEECRLLRNfSSVYAV 354

consensus 130 140 150 160 170 180
.....*.....|.....*.....|.....*.....|.....*.....|.....*.....|
101 VSALSSSPiSRlKKTWEKLpSKYKklFEELlELLDPSRNfKNYREALSSCN----- 151
RGL3      347 LSALQSNPIYRLKRSWGAVSREPLSTFRKLsQIFSDENNHLSSREILfQEEategsqeed 406
1BKD_S    270 VSAMNSSPVYRLDHTFEQIPsRQKKILEEAHELSE--DHYYKKYLAKLRsIN----- 318
gi 544403 467 LSALQSNAIHRLKKTWEeVSRGSFRVfQKLSEIFsdeNNYSLsRELLIKEGtskfatilem 526
gi 6919956 355 VSALQSSPIHRLRAAWGEATRDSLRVfSSLCQIFSeedNYsQSRELLVQEVklqspleph 414

consensus 190 200 210 220 230 240
.....*.....|.....*.....|.....*.....|.....*.....|.....*.....|
152 -----LPPCiPFLGVLLKDLTFIDEGNPdFLKN---GLVNfEKRRRKiAKIL 194
RGL3      407 n-----tpgslpskppPGVPVYLGTFLTDLVMLDTALpDMLEG---DLINfEKRRRKEWEIL 459
1BKD_S    319 -----PPCVpFFFGiYLTNIlKTEEGNPEVLKRhgkELINfSKRRKkVAEIT 363
gi 544403 527 nprrtqrqketgviQGTVPYLGTFLTDLVMLDTAMKDYLYG---RLINfEKRRRKEFEVI 583
gi 6919956 415 s----kkaprsrgsrgGGVVPYLGTFLTDLVMLDAAsKDELEN---GYINfDKRRRKEFAVL 467
```

FIG. 1



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**FIG. 1C**  
**RasGEF motif**  
**(Continued)**

	250	260	270	280	290	
	..... .....*..... .....*..... .....*..... .....*					
consensus	195 REIRQLQS--QPNLRPNRSDIQSLQQS--LDSLPEEN---ELYELSLRIEPRV	242				SEQ ID NO: 59
RGL3	460 ARIQQLQRrcQSYTLSPHPILAAL--HA--QNQLTEEQ----SYRLSRVIEPPa	506				SEQ ID NO: 60
1BKD_S	364 GEIQYQN--QPYCLRVE--SDIKRFFENLpMGNSMEKEftdYLFNKSLEIEPRN	415				SEQ ID NO: 61
gi 544403	584 AQIKLLQsacNNYSIVPE--EHFGAWFRAM---GRLSEA----ESYNLSCELEPPS	630				SEQ ID NO: 62
gi 6919956	468 SELRRLLQnecRGYNLQPD-HDIQRWLQG---LRPLTEA----QSHRVSCVEVEPPG	514				SEQ ID NO: 63

**FIG. 1D**  
**RA motif**

	10	20	30	40	50	60	
	..... .....*..... .....*..... .....*..... .....*.....						
consensus	1 DQGVLRVYFQDLKPGVAYKTIrVSSSEDtAPDVVQlALEKFRlDDEDPEEYALVEVLSGDK	60					
RGL3	613 earVIRVSiDNDH-GNLYRSiLLTSQDKAPSVRRALQKHNVQPWACDYQLFQVLPGDR	671					
1EF5_A	17 DTCiIRiSVEDn-NGNMYKSiMLTSQDKTPAViQRAMSKHNLESdPAEEYELVQViSEDK	75					
1RLF	4 DCRIiRVQMeLgeDGSVYKSiLVTSQDKAPSViSRVLKKNRDSAVASEFELVQLLPGDR	63					
1LXD_A	15 DCCiIRVSLDVd-NGNMYKSiLVTSQDKAPTViRKAMDKHNLDDEPEdYELLQIiSEdH	73					

  

	70	80	90	
	..... .....*..... .....*..... ...			
consensus	61 ERKLpDDENPLQLRLNLPRDGLSLRFLlKRrD	92	SEQ ID NO: 64	
RGL3	672 VLLiPDNANVFYAM----SPVAPRDFMLRRKE	699	SEQ ID NO: 65	
1EF5_A	76 ELViPDSANVFYAMNSQVN----FDfILRKKN	103	SEQ ID NO: 66	
1RLF	64 ELTiPHSANVFYAMDGAS-----HDfLLRQRr	90	SEQ ID NO: 67	
1LXD_A	74 KLKiPENANVFYAMNSAAN-----YDfILKKR-	100	SEQ ID NO: 68	

**FIG. 1**



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# Structure of RGL3 and alignment of RasGEFN, RasGEF and RA motifs.

**FIG. 1A**  
RGL3 (710 a.a.)





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**FIG. 1B**  
**RasGEFN motif**

	10	20	30	40	50	60
consensus	.....*..... .....*..... .....*..... .....*..... .....*.....					
RGL3	1 CKGGLIKGGTLEKLIIEHLTEARDK-VDPFTFVEFTLLTYRSFITTQELLQKLLYRYNAIPP	59				
gi 1354501	64 SKVRVLRAARLERLVGELVFGDRE-QDPSPMPAFATYRTFVPTACLLGFLLP--PMPPP	120				
gi 158471	87 RSSRRLRAGTLEALVRHLLDARTAGADMFTPALLATHRRAFTSTPALFGLVADRLEALES	146				
gi 544403	636 AGVPMIKGATLCKLIERLTYHIY--ADPTFVRTFLTTRYFYFCSPQQLQLLVERFNIPDP	693				
	111 CKVRTVKAGTLEKLVVEHLVPAFQg-SDLSYVTVFLCTVRAFTTTTQQVLDLLFKRYGCILP	169				
	70	80	90	100	110	120
consensus	.....*..... .....*..... .....*..... .....*..... .....*.....					
RGL3	60 EGVE-----D-----D-----IWVKEKVNPRRIQ---NRVLNILRLWV	88				
gi 1354501	121 PPPG-----V-----EIKKTAVQDLSFNknlRAVSVLGSWL	152				
gi 158471	147 Y-----PPGELERTT---GVAISVLSTWL	167				
gi 544403	694 SLVYqdtgtagagmgvggDkehknshredwkRYRKEYVQP--VQ---FRVLNVLRHWV	748				
	170 Yss-----eDg-----GPQDQLK---NAISSILGTWL	193				
	130	140	150	160		
consensus	.....*..... .....*..... .....*..... .....*..... .....*.....					
RGL3	89 ENYWQDFEEDPKNLNLFLEE-FLELVDDK-KYPGLETSLQNILRRLS	132				
gi 1354501	153 QDHPQDFRDHPahsdlgsvrtflgwaapgsaeaklledflee	198				
gi 158471	168 ASHPEDFGSEVKGQLDRLE-SFLLRGTGYaAREGVVGGADLIRNLR	212				
gi 544403	749 DHHFYDFEKDPMLEKLLN-FLEHVNGK-SMRKWVDSVLKIVQRKN	792				
	194 DQYSEDFCQP-PDFPCLKQLVAYVQLNM-PGSDLERRAHLLLAQLE	237				



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**FIG. 1C**  
**RasGEF motif**

	10	20	30	40	50	60		
	.....*	.....*	.....*	.....*	.....*	.....*		
consensus	1	LLLLDPKELAEQ	LTLLDFELFRKID	PSSELLGSVWGKRSKKS	--PSPL--	NLERFIERFNE	56	
RGL3	243	LLDFSDEVAEQ	LTLLIDLELFSK	VRLYECLGSVWSQDRPGaaGASP	--TVRATVAQFNT		300	
1BKD_S	171	LLTLHPIEIARQ	LTLLLESDLYRAV	QPSSELVGSVWTKEDKEI	--NSP--	NLLKMIRHTTN	225	
gi 544403	363	LLLFPDPLVAEQ	FTLLMDAELFKK	VVPYHCLGSISQRAKKG	--KEHlapTIRATVAQFNN		420	
gi 6919956	239	VLVFLADHLAEQ	LTLLDAELFLNLI	PSQCLGGLWGHDRPG	--HSHlcpSVRATVTQFNK		296	
	70	80	90	100	110	120		
	.....*	.....*	.....*	.....*	.....*	.....*		
consensus	57	VSNWVATEILKQT	T-----P--	KDRAELLSKFIQVAKHCRELN	NFNLSLMAI		100	
RGL3	301	VTGCVLGSVLGAP	G-----Laa	PQRAQRLEKWIRIAQRCREL	RNFSSLRAl		346	
1BKD_S	226	LTLMFEKCI	VETEN-----L--	EERVAVVSRIIEILQVFQEL	NNFNGLVLEV		269	
gi 544403	421	VANCVITTC	LDGDSm-----ka--	SDRARVVEHWIEVARECR	VLNKFNSSLYAI		466	
gi 6919956	297	VAGAVVSSVLG	ATStgepgpgevtir	lprP--PQARALLEKWIRV	AEERLLRNFSVYAV		354	
	130	140	150	160	170	180		
	.....*	.....*	.....*	.....*	.....*	.....*		
consensus	101	VSALSSSPI	SRLKKTWEKLP	SKYKKLFEELEELL	DPSRNFKNYREALSSCN	-----	151	
RGL3	347	LSALQSNPI	YRLKRSWGAVS	REPLSTFRKLSQIFSDENN	HLSSREILFQEEategs	qeed	406	
1BKD_S	270	VSAMNSSPV	YRLDHTFEQIP	SRQKKILEEAHELSE	--DHYKKYLA	KLRSIN-----	318	
gi 544403	467	LSALQSNAI	HRLLKKTWEEV	SRGSFRVFQKLSEIF	SdeNNYSLSRELLI	KEGtskfatem	526	
gi 6919956	355	VSALQSSPI	HRLLRAAWGEAT	RDSLRFVSSLCQIF	SeedNYSQSRELLV	QEVklqsp	414	
	190	200	210	220	230	240		
	.....*	.....*	.....*	.....*	.....*	.....*		
consensus	152	-----LPPC	IPFLGVLLKDL	TFIDEGNP	DFLKN--GLVNF	EKRKRKIAKIL	194	
RGL3	407	n-----tpg	slpskppPGVP	YLGTF	FLTDLVMLD	TALPDMLEG---	DLINFEKRRKEWEIL	459
1BKD_S	319	-----PPC	VFFGIYLTN	ILKTEEGN	PEVLKRhgkelIN	FSKRRKVAEIT	363	
gi 544403	527	nprrtqrrq	ketgviQGT	VPYLGTF	FLTDLVMLD	TAMKDYLG---	RLINFEKRRKEFEVI	583
gi 6919956	415	s-----kka	prsgsrgGGV	VPYLGTF	FLKDLVMLD	AASKDELEN---	GYINFDKRRKEFAVL	467



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## FIG. 1C

### RasGEF motif

(Continued)

consensus	195	REIRQLQS--QPNLRPNRSDIQSLQQS--LDSLPEEN---	242	SEQ ID NO: 59
RGL3	460	ARIQQLQRrcQSYTLSPHPILAAL--HA--QNQLTEEQ----	506	SEQ ID NO: 60
1BKD_S	364	GEIQQYQN--QPYCLRVE-SDIKRFFENLpMGNSMEKEftdYLFNKSLEIEPRN	415	SEQ ID NO: 61
gi 544403	584	AQIKLLQSacNNYSIVPE-EHFGAWFRAM---GRLSEA-----	630	SEQ ID NO: 62
gi 6919956	468	SELRRQLNecRGYNLQPD-HDIQRWLQG---LRPLTEA---QSHRVSCVEVEPPG	514	SEQ ID NO: 63

## FIG. 1D

### RA motif

consensus	1	DQGVLRVYFQDLKPGVAYKTIrVSSedTAPDVVQLALEKFRLDDEDPEEYALVEVLSGDK	60
RGL3	613	earVIRVSiDNDH-GNLYRSiLLTSQDKAPSVVRRALQKHNVQPWACDYQLFQVLPGDR	671
1EF5_A	17	DTcIIIRiSVEdn-NGNMYKSIMLTsQDKTPAVIQRAMSKHNLESDPAEEYELVQVISEDK	75
1RLF	4	DCRIIRVQMeLgeDGSVYKSILVTSQDKAPSVISrVLKKNRDSAVASEFELVQLLPGDR	63
1LXD_A	15	DCCIIRVSLDVd-NGNMYKSILVTSQDKAPTVirKAMDKHNLDedePEdYELLQIIISEDH	73

consensus	61	ERKLpDDENPLQLRLNLPDGLSLRFLKRRD	92	SEQ ID NO: 64
RGL3	672	VLLIPDNANVFYAM----SPVAPRDFMLRRKE	699	SEQ ID NO: 65
1EF5_A	76	ELVIPDSANVFYAMNSQVN----FDFILRKKN	103	SEQ ID NO: 66
1RLF	64	ELTIpHSANVFYAMDGAS-----HDFLLRQRR	90	SEQ ID NO: 67
1LXD_A	74	KLKIPENANVFYAMNSAAN-----YDFILKRR-	100	SEQ ID NO: 68